

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown as a strike through, and inserted material is shown as underlined.

In the Claims

Claims 172-174 and 176 have been amended as follows:

172. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (b) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (b) an isolated

nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; wherein expression of the chimeric gene results in an altered corn stearic acid phenotype.

173. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (b) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; wherein expression of the chimeric gene results in an altered corn oleic acid phenotype.

174. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (c) an isolated nucleic acid fragment comprising a corn oleosin promoter

wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences,

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or the reverse complement thereof, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or the reverse complement thereof, (c) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, and (d) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, wherein expression of the chimeric gene results in an altered corn oil phenotype.

176. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises

(i) a first chimeric gene selected from the group consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (BB) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (2) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (3) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, and

(ii) a second chimeric gene selected from the set consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, and (2) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment thereof, or the reverse complement of either the fragment or subfragment, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment comprising a full length or partial corn oleosin promoter hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (3) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, wherein expression of the chimeric genes results in an altered corn oil phenotype.